Abstract

Cortisol is a stress hormone that is regulated by the hypothalamic pituitary adrenal axis which is impacted by both circadian rhythms and acute stress. If stress becomes chronic, cortisol levels in the body continually rise instead of having natural oscillations, which can predispose individuals to compromised physical and mental health. Since stress hormone receptors play a role in gene regulatory networks, the effects of chronic stress can be seen through studying gene expression. The effects of chronic stress on zebrafish were investigated by exposing embryos to cortisol and studying the ability of those adults to respond to a stressor later in life (tailfin amputation) using bulk genomics methods (Hartig et al., 2016). However, the main limitation of bulk genomics methods is the loss of single cell resolution. This means that observed differential gene expression patterns could either be due to true differences in gene expression as a response to treatment, or due to the growth patterns of different cell types since each cell expresses a unique transcriptome.

Previous work understanding the cellular diversity of the caudal fin and the impacts of chronic early life stress on the regeneration of the caudal fin come together in the present study to indicate what cell types of the regenerating caudal fin are impacted by chronic early-life stress. The goal of this research is to explore the differential cellular responses in adult zebrafish to chronic early life stress by studying the regenerating tailfin. The results reported here indicate that overall, hematopoietic cells in adult zebrafish are most effected by the chronic exposure to cortisol in early development. In addition, these results demonstrate the usefulness of single cell genomics methods to provide cell type context to previously collected bulk genomic data.